

SEQUENCE LISTING

<110> Bartel, Paul L.
Tavtigian, Sean V.
Myriad Genetics, Inc.

<120> MMSC1 - An MMAC1 Interacting Protein

<130> MMSC1 Gene

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<150> US 60/071,861

<151> 1998-01-20

<160> 65

<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:PDZ Consensus
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3 may be any amino acid; Xaa at residue 4 may be
Val or Ile.

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130 135 140

Leu Gly Phe Ser Val Val Ala Leu Arg Ser Gln Asn Leu Gly Lys Val
145 150 155 160

Asp Ile Phe Val Lys Asp Val Gln Pro Gly Ser Val Ala Asp Arg Asp
165 170 175

Gln Arg Leu Lys Glu Asn Asp Gln Ile Leu Ala Ile Asn His Thr Pro
180 185 190

Leu Asp Gln Asn Ile Ser His Gln Gln Ala Ile Ala Leu Leu Gln Gln
195 200 205

Thr	Thr	Gly	Ser	Leu	Arg	Leu	Ile	Val	Ala	Arg	Glu	Pro	Val	His	Thr	210	215	220
Lys	Ser	Ser	Thr	Ser	Ser	Ser	Leu	Asn	Asp	Thr	Thr	Leu	Pro	Glu	Thr	225	230	235 240
Val	Cys	Trp	Gly	His	Val	Glu	Glu	Val	Glu	Leu	Ile	Asn	Asp	Gly	Ser	245	250	255
Gly	Leu	Gly	Phe	Gly	Ile	Val	Gly	Gly	Lys	Thr	Ser	Gly	Val	Val	Val	260	265	270
Arg	Thr	Ile	Val	Pro	Gly	Gly	Leu	Ala	Asp	Arg	Asp	Gly	Arg	Leu	Gln	275	280	285
Thr	Gly	Asp	His	Ile	Leu	Lys	Ile	Gly	Gly	Thr	Asn	Val	Gln	Gly	Met	290	295	300
Thr	Ser	Glu	Gln	Val	Ala	Gln	Val	Leu	Arg	Asn	Cys	Gly	Asn	Ser	Val	305	310	315 320
Arg	Met	Leu	Val	Ala	Arg	Asp	Pro	Ala	Gly	Asp	Ile	Ser	Val	Thr	Pro	325	330	335
Pro	Ala	Pro	Ala	Ala	Leu	Pro	Val	Ala	Leu	Pro	Thr	Val	Ala	Ser	Lys	340	345	350
Gly	Pro	Gly	Ser	Asp	Ser	Ser	Leu	Phe	Glu	Thr	Tyr	Asn	Val	Glu	Leu	355	360	365
Val	Arg	Lys	Asp	Gly	Gln	Ser	Leu	Gly	Ile	Arg	Ile	Val	Gly	Tyr	Val	370	375	380
Gly	Thr	Ser	His	Thr	Gly	Glu	Ala	Ser	Gly	Ile	Tyr	Val	Lys	Ser	Val	385	390	395 400
Ile	Pro	Gly	Ser	Ala	Ala	Tyr	His	Asn	Gly	His	Ile	Gln	Val	Asn	Asp	405	410	415
Lys	Ile	Val	Ala	Val	Asp	Gly	Val	Asn	Ile	Gln	Gly	Phe	Ala	Asn	His	420	425	430
Asp	Val	Val	Glu	Val	Leu	Arg	Asn	Ala	Gly	Gln	Val	Val	His	Leu	Thr	435	440	445
Leu	Val	Arg	Arg	Lys	Thr	Ser	Ser	Ser	Thr	Ser	Pro	Leu	Glu	Pro	Pro	450	455	460
Ser	Asp	Arg	Gly	Thr	Val	Val	Glu	Pro	Leu	Lys	Pro	Pro	Ala	Leu	Phe	465	470	475 480
Leu	Thr	Gly	Ala	Val	Glu	Thr	Glu	Thr	Asn	Val	Asp	Gly	Glu	Asp	Glu	485	490	495
Glu	Ile	Lys	Glu	Arg	Ile	Asp	Thr	Leu	Lys	Asn	Asp	Asn	Ile	Gln	Ala	500	505	510
Leu	Glu	Lys	Leu	Glu	Lys	Val	Pro	Asp	Ser	Pro	Glu	Asn	Glu	Leu	Lys	515	520	525
Ser	Arg	Trp	Glu	Asn	Leu	Leu	Gly	Pro	Asp	Tyr	Glu	Val	Met	Val	Ala	530	535	540

Thr	Leu	Asp	Thr	Gln	Ile	Ala	Asp	Asp	Ala	Glu	Leu	Gln	Lys	Tyr	Ser	545	550	555	560
Lys	Leu	Leu	Pro	Ile	His	Thr	Leu	Arg	Leu	Gly	Val	Glu	Val	Asp	Ser	565	570	575	
Phe	Asp	Gly	His	His	Tyr	Ile	Ser	Ser	Ile	Val	Ser	Gly	Gly	Pro	Val	580	585	590	
Asp	Thr	Leu	Gly	Leu	Leu	Gln	Pro	Glu	Asp	Glu	Leu	Leu	Glu	Val	Asn	595	600	605	
Gly	Met	Gln	Leu	Tyr	Gly	Lys	Ser	Arg	Arg	Glu	Ala	Val	Ser	Phe	Leu	610	615	620	
Lys	Glu	Val	Pro	Pro	Pro	Phe	Thr	Leu	Val	Cys	Cys	Arg	Arg	Leu	Phe	625	630	635	640
Asp	Asp	Glu	Ala	Ser	Val	Asp	Glu	Pro	Arg	Arg	Thr	Glu	Thr	Ser	Leu	645	650	655	
Pro	Glu	Thr	Glu	Val	Asp	His	Asn	Met	Asp	Val	Asn	Thr	Glu	Glu	Asp	660	665	670	
Asp	Asp	Gly	Glu	Leu	Ala	Leu	Trp	Ser	Pro	Glu	Val	Lys	Ile	Val	Glu	675	680	685	
Leu	Val	Lys	Asp	Cys	Lys	Gly	Leu	Gly	Phe	Ser	Ile	Leu	Asp	Tyr	Gln	690	695	700	
Asp	Pro	Leu	Asp	Pro	Thr	Arg	Ser	Val	Ile	Val	Ile	Arg	Ser	Leu	Val	705	710	715	720
Ala	Asp	Gly	Val	Ala	Glu	Arg	Ser	Gly	Gly	Leu	Leu	Pro	Gly	Asp	Arg	725	730	735	
Leu	Val	Ser	Val	Asn	Glu	Tyr	Cys	Leu	Asp	Asn	Thr	Ser	Leu	Ala	Glu	740	745	750	
Ala	Val	Glu	Ile	Leu	Lys	Ala	Val	Pro	Pro	Gly	Leu	Val	His	Leu	Gly	755	760	765	
Ile	Cys	Lys	Pro	Leu	Val	Glu	Asp	Asn	Glu	Glu	Glu	Ser	Cys	Tyr	Ile	770	775	780	
Leu	His	Ser	Ser	Ser	Asn	Glu	Asp	Lys	Thr	Glu	Phe	Ser	Gly	Thr	Ile	785	790	795	800
His	Asp	Ile	Asn	Ser	Ser	Leu	Ile	Leu	Glu	Ala	Pro	Lys	Gly	Phe	Arg	805	810	815	
Asp	Glu	Pro	Tyr	Phe	Lys	Glu	Glu	Leu	Val	Asp	Glu	Pro	Phe	Leu	Asp	820	825	830	
Leu	Gly	Lys	Ser	Phe	His	Ser	Gln	Gln	Lys	Glu	Ile	Glu	Gln	Ser	Lys	835	840	845	
Glu	Ala	Trp	Glu	Met	His	Glu	Phe	Leu	Thr	Pro	Arg	Leu	Gln	Glu	Met	850	855	860	
Asp	Glu	Glu	Arg	Glu	Met	Leu	Val	Asp	Glu	Glu	Tyr	Glu	Leu	Tyr	Gln	865	870	875	880

Asp Pro Ser Pro Ser Met Glu Leu Tyr Pro Leu Ser His Ile Gln Glu
 885 890 895
 Ala Thr Pro Val Pro Ser Val Asn Glu Leu His Phe Gly Thr Gln Trp
 900 905 910
 Leu His Asp Asn Glu Pro Ser Glu Ser Gln Glu Ala Arg Thr Gly Arg
 915 920 925
 Thr Val Tyr Ser Gln Glu Ala Gln Pro Tyr Gly Tyr Cys Pro Glu Asn
 930 935 940
 Val Met Lys Glu Asn Phe Val Met Glu Ser Leu Pro Ser Val Pro Ser
 945 950 955 960
 Thr Glu Gly Asn Ser Gln Gln Gly Arg Phe Asp Asp Leu Glu Asn Leu
 965 970 975
 Asn Ser Leu Ala Lys Thr Ser Leu Asp Leu Gly Met Ile Pro Asn Asp
 980 985 990
 Val Gln Gly Pro Ser Leu Leu Ile Asp Leu Pro Val Val Ala Gln Arg
 995 1000 1005
 Arg Glu Gln Glu Asp Leu Pro Leu Tyr Gln His Gln Ala Thr Arg Val
 1010 1015 1020
 Ile Ser Lys Ala Ser Ala Tyr Thr Gly Met Leu Ser Ser Arg Tyr Ala
 025 1030 1035 1040
 Thr Asp Thr Cys Glu Leu Pro Glu Arg Glu Glu Gly Glu Gly Glu Glu
 1045 1050 1055
 Thr Pro Asn Phe Ser His Trp Gly Pro Pro Arg Ile Val Glu Ile Phe
 1060 1065 1070
 Arg Glu Pro Asn Val Ser Leu Gly Ile Ser Ile Val Gly Gly Gln Thr
 1075 1080 1085
 Val Ile Lys Arg Leu Lys Asn Gly Glu Glu Leu Lys Gly Ile Phe Ile
 1090 1095 1100
 Lys Gln Val Leu Glu Asp Ser Pro Ala Gly Lys Thr Asn Ala Leu Lys
 105 1110 1115 1120
 Thr Gly Asp Lys Ile Leu Glu Val Ser Gly Val Asp Leu Gln Asn Ala
 1125 1130 1135
 Ser His Ser Glu Ala Val Glu Ala Ile Lys Asn Ala Gly Asn Pro Val
 1140 1145 1150
 Val Phe Ile Val Gln Ser Leu Ser Ser Thr Pro Arg Val Ile Pro Asn
 1155 1160 1165
 Val His Asn Lys Ala Asn Lys Ile Thr Ser Asn Gln Asn Gln Asp Thr
 1170 1175 1180
 Gln Glu Lys Lys Glu Lys Arg Gln Gly Thr Ala Pro Pro Pro Met Lys
 185 1190 1195 1200
 Leu Pro Pro Pro Tyr Lys Ala Leu Thr Asp Asp Ser Asp Glu Asn Glu
 1205 1210 1215

Glu Glu Asp Ala Phe Thr Asp Gln Lys Ile Arg Gln Arg Tyr Ala Asp
1220 1225 1230

Leu Pro Gly Glu Leu His Ile Ile Glu Leu Glu Lys Asp Lys Asn Gly
1235 1240 1245

Leu Gly Leu Ser Leu Ala Gly Asn Lys Asp Arg Ser Arg Met Ser Ile
1250 1255 1260

Phe Val Val Gly Ile Asn Pro Glu Gly Pro Ala Ala Ala Asp Gly Arg
265 1270 1275 1280

Met His Ile Gly Asp Glu Leu Leu Glu Ile Asn Asn Gln Ile Leu Tyr
1285 1290 1295

Gly Arg Ser His Gln Asn Ala Ser Ala Ile Ile Lys Thr Ala Pro Ser
1300 1305 1310

Lys Val Lys Leu Val Phe Ile Arg Asn Glu Asp Ala Val Asn Gln Met
1315 1320 1325

Ala Val Thr Pro Phe Pro Val Pro Ser Ser Ser Pro Ser Ser Ile Glu
1330 1335 1340

Asp Gln Ser Gly Thr Glu Pro Ile Ser Ser Glu Glu Asp Gly Ser Leu
345 1350 1355 1360

Glu Val Gly Ile Lys Gln Leu Pro Glu Ser Glu Ser Phe Lys Leu Ala
1365 1370 1375

Val Ser Gln Met Lys Gln Gln Lys Tyr Pro Thr Lys Val Ser Phe Ser
1380 1385 1390

Ser Gln Glu Ile Pro Leu Ala Pro Ala Ser Ser Tyr His Ser Thr Asp
1395 1400 1405

Ala Asp Phe Thr Gly Tyr Gly Gly Phe Gln Ala Pro Leu Ser Val Asp
1410 1415 1420

Pro Ala Thr Cys Pro Ile Val Pro Gly Gln Glu Met Ile Ile Glu Ile
425 1430 1435 1440

Ser Lys Gly Arg Ser Gly Leu Gly Leu Ser Ile Val Gly Gly Lys Asp
1445 1450 1455

Thr Pro Leu Asn Ala Ile Val Ile His Glu Val Tyr Glu Glu Gly Ala
1460 1465 1470

Ala Ala Arg Asp Gly Arg Leu Trp Ala Gly Asp Gln Ile Leu Glu Val
1475 1480 1485

Asn Gly Val Asp Leu Arg Asn Ser Ser His Glu Glu Ala Ile Thr Ala
1490 1495 1500

Leu Arg Gln Thr Pro Gln Lys Val Arg Leu Val Val Tyr Arg Asp Glu
505 1510 1515 1520

Ala His Tyr Arg Asp Glu Glu Asn Leu Glu Ile Phe Pro Val Asp Leu
1525 1530 1535

Gln Lys Lys Ala Gly Arg Gly Leu Gly Leu Ser Ile Val Gly Lys Arg
1540 1545 1550

Asn Gly Ser Gly Val Phe Ile Ser Asp Ile Val Lys Gly Gly Ala Ala
1555 1560 1565

Asp Leu Asp Gly Arg Leu Ile Gln Gly Asp Gln Ile Leu Ser Val Asn
1570 1575 1580

Gly Glu Asp Met Arg Asn Ala Ser Gln Glu Thr Val Ala Thr Ile Leu
585 1590 1595 1600

Lys Cys Ala Gln Gly Leu Val Gln Leu Glu Ile Gly Arg Leu Arg Ala
1605 1610 1615

Gly Ser Trp Thr Ser Ala Arg Thr Thr Ser Gln Asn Ser Gln Gly Ser
1620 1625 1630

Gln Gln Ser Ala His Ser Ser Cys His Pro Ser Phe Ala Pro Val Ile
1635 1640 1645

Thr Gly Leu Gln Asn Leu Val Gly Thr Lys Arg Val Ser Asp Pro Ser
1650 1655 1660

Gln Lys Asn Ser Gly Thr Asp Met Glu Pro Arg Thr Val Glu Ile Asn
665 1670 1675 1680

Arg Glu Leu Ser Asp Ala Leu Gly Ile Ser Ile Ala Gly Gly Arg Gly
1685 1690 1695

Ser Pro Leu Gly Asp Ile Pro Val Phe Ile Ala Met Ile Gln Ala Ser
1700 1705 1710

Gly Val Ala Ala Arg Thr Gln Lys Leu Lys Val Gly Asp Arg Ile Val
1715 1720 1725

Ser Ile Asn Gly Gln Pro Leu Asp Gly Leu Ser His Ala Asp Val Val
1730 1735 1740

Asn Leu Leu Lys Asn Ala Tyr Gly Arg Ile Ile Leu Gln Val Val Ala
745 1750 1755 1760

Asp Thr Asn Ile Ser Ala Ile Ala Ala Gln Leu Glu Asn Met Ser Thr
1765 1770 1775

Gly Tyr His Leu Gly Ser Pro Thr Ala Glu His His Pro Glu Asp Thr
1780 1785 1790

Glu Thr Pro Pro Pro Lys Ile Ile Thr Leu Glu Lys Gly Ser Glu Gly
1795 1800 1805

Leu Gly Phe Ser Ile Val Gly Gly Tyr Gly Ser Pro His Gly Asp Leu
1810 1815 1820

Pro Ile Tyr Val Lys Thr Val Phe Ala Lys Gly Ala Ala Ala Asp Asp
825 1830 1835 1840

Gly Arg Leu Lys Arg Gly Asp Gln Ile Leu Ala Val Asn Gly Glu Thr
1845 1850 1855

Leu Glu Gly Val Thr His Glu Gln Ala Val Ala Ile Leu Lys His Gln
1860 1865 1870

Arg Gly Thr Val Thr Leu Thr Val Leu
1875 1880

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 <211> 290
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 <213> Mus musculus

<220>
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<400> 4
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 gcccgatcag acttttttga agtgattgaa aagaatatcc caaa atg cct gaa aac 116
 Met Pro Glu Asn
 1
 cct gct gca gag aag atg cag gtc ctg cag gtc ctg gat cgc ctt cga 164
 Pro Ala Ala Glu Lys Met Gln Val Leu Gln Val Leu Asp Arg Leu Arg
 5 10 15 20
 ggg aag ctg cag gag aag gga gac acg acg cag aac gag aag ctg tct 212
 Gly Lys Leu Gln Glu Lys Gly Asp Thr Thr Gln Asn Glu Lys Leu Ser
 25 30 35
 ggg ttc tac gag acg ctg aag agc cct ctc ttc aac cag atc ctt aca 260
 Ala Phe Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn Gln Ile Leu Thr
 40 45 50
 ctg cag cag tcc atc aag cag ctg aag gga 290
 Leu Gln Gln Ser Ile Lys Gln Leu Lys Gly
 55 60

<210> 5
 <211> 62
 <212> PRT
 <213> Mus musculus

<400> 5
 Met Pro Glu Asn Pro Ala Ala Glu Lys Met Gln Val Leu Gln Val Leu
 1 5 10 15
 Asp Arg Leu Arg Gly Lys Leu Gln Glu Lys Gly Asp Thr Thr Gln Asn
 20 25 30
 Glu Lys Leu Ser Ala Phe Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn
 35 40 45
 Gln Ile Leu Thr Leu Gln Gln Ser Ile Lys Gln Leu Lys Gly
 50 55 60

<210> 6
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 6
 Asn Glu Pro Phe Asp Glu Asp Gln His Thr Gln Ile Thr Lys Val
 1 5 10 15

<210> 7
 <211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:SH3 Binding
Protein PDZ Domain

<400> 7
Ser Gly Ser Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg
1 5 10 15

<210> 8
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:AF6 PDZ Binding
Protein

<400> 8
Ser Gly Asp Asp Gly Asp Asp Pro Phe Leu Gln Tyr Glu Phe Tyr Val
1 5 10 15

<210> 9
<211> 16
<212> PRT
<213> Homo sapiens

<400> 9
Glu Asn Glu Pro Phe Asp Glu Asp Gln His Thr Gln Ile Thr Lys Val
1 5 10 15

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MMSC1 Primers

<400> 10
caggtgaggc agggccgaca 20

<210> 11
<211> 22
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 11
ctacagtagg cagggcaaca gg 22

<210> 12
<211> 38
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MMSC1 Primers

<400> 12

gttttcccag tcacgacgcg ggctcccacc tgctcctc

38

<210> 13

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MMSC1 Primers

<400> 13

aggaaacagc tatgaccatg tgaacactaa caaacctttc c

41

<210> 14

<211> 40

<212> DNA

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gttttcccag tcacgacgtc aactcaacca tataccctca

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<400> 15

aggaaacagc tatgaccatg gctggacatc cttcacgaag

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<210> 16

<211> 38

<212> DNA

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<400> 16

gttttcccag tcacgacggc ctgggattca gtgtgggtg

38

<210> 17

<211> 40

<212> DNA

<213> Artificial Sequence

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aggaaacagc tatgaccatc cccaacaaac tgtttcaggc 40

<210> 18
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<400> 18
gttttcccag tcacgacgcc agggaaccag tccacaca 38

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<400> 19
aggaaacagc tatgaccatc ctgactgaat tcccacag 38

<210> 20
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<400> 20
tcctggagga ttagcagatc gag 23

<210> 21
<211> 24
<212> DNA
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<400> 21
ggtaatccaa aatgctgaat ccca 24

<210> 22
<211> 39
<212> DNA
<213> Artificial Sequence

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gttttcccag tcacgacgaa gattggtggc acaaacgtg 39

<210> 23

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aggaaacagc tatgaccata gcaactgccag gtattatact t 41

<210> 24
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<400> 24
gttttcccag tcacgacgag aattgttggc tatgttggaa c 41

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<400> 25
aggaaacagc tatgaccatg ctccagttag aaagagagct g 41

<210> 26
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<400> 26
gttttcccag tcacgacgac atctcatct acttctcca 39

<210> 27
<211> 40
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<400> 27
aggaaacagc tatgaccata actcagcatc atctgcaatc 40

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<400> 28
gttttcccag tcacgacggg aaaacctgtt gggtcctg 38

<210> 29
<211> 42
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<213> Artificial Sequence

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<210> 30
<211> 22
<212> DNA
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<400> 30
gtggattcct ttgatgggca cc 22

<210> 31
<211> 23
<212> DNA
<213> Artificial Sequence

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<400> 31
ctttgagcca caacaggaag gtc 23

<210> 32
<211> 39
<212> DNA
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<220>
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<400> 32
gttttcccag tcacgacgtg agctgottga ggtcaatgg 39

<210> 33
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<212> DNA
<213> Artificial Sequence

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<400> 33

aggaaacagc tatgaccatc taaagggtcc tggtaatcc 39

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<223> Description of Artificial Sequence:MMSC1 Primers

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<211> 44
<212> DNA
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<223> Description of Artificial Sequence:MMSC1 Primers

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<210> 36
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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 36
gttttcccag tcacgacgga aatattgaaa gctgtgcc 38

<210> 37
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<210> 38
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gttttcccag tcacgacgaa agtctttcca ttcccaacaa 40

<210> 39

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<400> 39
aggaaacagc tatgaccatc catacggctg tgcctcctg 39

<210> 40
<211> 25
<212> DNA
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<220>
<223> Description of Artificial Sequence:MMSC1 Primers

<400> 40
gagttatata aagatccctc accat 25

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MMSC1 Primers

<400> 41
caaatatgct catgcgtgat cgg 23

<210> 42
<211> 41
<212> DNA
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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 42
gttttcccag tcacgacgtt cactttggta cacagtggtt g 41

<210> 43
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<400> 43
aggaaacagc tatgaccata aatcttcttg ctccctcctt 40

<210> 44
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<400> 44

gttttcccag tcacgacgcc cgaatgatgt ccaaggtcc

39

<210> 45

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MMSC1 Primers

<400> 45

aggaaacagc tatgaccatg tccaccaaca atactgatcc

40

<210> 46

<211> 38

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 46

gttttcccag tcacgacgag ccaactggggt ccaccgag

38

<210> 47

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MMSC1 Primers

<400> 47

aggaaaacagc tatgaccata ctcgtggagt ggatgacaaa c

41

<210> 48

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MMSC1 Primers

<400> 48

gttttcccag tcacgacgca gttgaggcca ttaagaat

38

<210> 49

<211> 42

<212> DNA

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<400> 49

aggaaacagc tatgaccatc aagttcaata atgtgcagtt ct 42

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MMSC1 Primers

<400> 50
cgccaatgaa acttcctcct cct 23

<210> 51
<211> 23
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MMSC1 Primers

<400> 51
tctcctgtga ggcatttctc atg 23

<210> 52
<211> 41
<212> DNA
<213> Artificial Sequence

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<400> 52
gttttcccag tcacgacgcc tttaccgacc aaaaaatcag a 41

<210> 53
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<212> DNA
<213> Artificial Sequence

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<400> 53
aggaaacagc tatgaccatc tgattgactg catcctcg 38

<210> 54
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MMSC1 Primers

<400> 54
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<211> 41
<212> DNA
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<220>
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<400> 55
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<400> 57
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<210> 62
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<400> 63
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<400> 65

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aggaaacagc tatgaccatt acccacatcc gcgtgagac

39